

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1552	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:43
L2	231063	conserv\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44
L3	11569	capsid	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44
L4	164	I1 and I2 and I3	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44



# results of BLAST

BLASTN 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1149884911-10709-74675597701.BLASTQ1

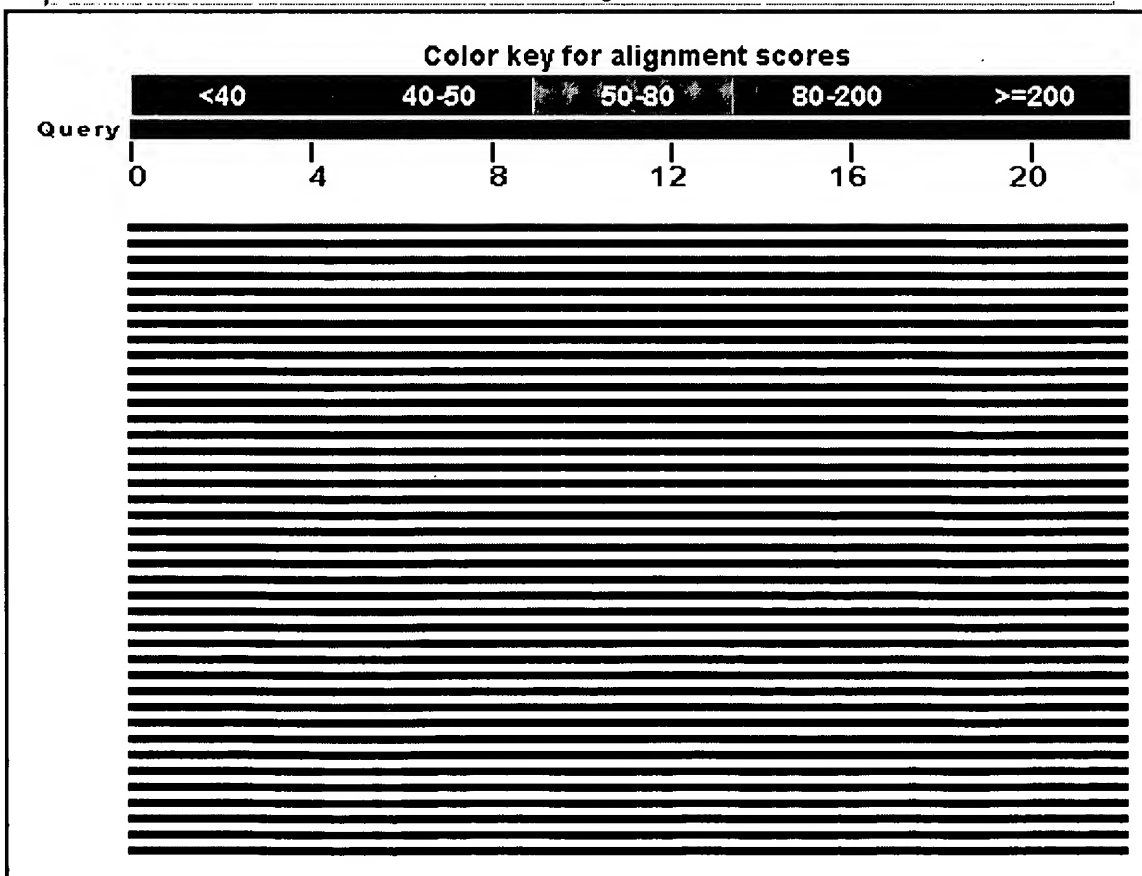
**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
3,946,763 sequences; 17,323,791,715 total letters

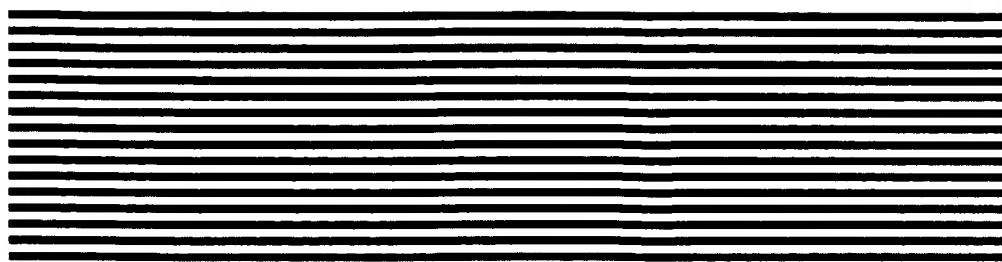
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**  
Length=22

## Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments





Tree view 

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 55975602 gb AY660002.1 </a>	West Nile virus isolate Mex03 from Me		44.1	0.004
<a href="#">gi 55495180 gb AY712948.1 </a>	West Nile virus isolate Mosquito v436		44.1	0.004
<a href="#">gi 55495165 gb AY712947.1 </a>	West Nile virus isolate Bird 1461, co		44.1	0.004
<a href="#">gi 55495149 gb AY712946.1 </a>	West Nile virus isolate Bird 1171, co		44.1	0.004
<a href="#">gi 55495130 gb AY712945.1 </a>	West Nile virus isolate Bird 1153, co		44.1	0.004
<a href="#">gi 51095221 gb AY688948.1 </a>	West Nile virus strain Sarafend, comp		44.1	0.004
<a href="#">gi 77980183 gb AY848696.2 </a>	West Nile virus strain 385-99 isol...		44.1	0.004
<a href="#">gi 77980181 gb AY848695.2 </a>	West Nile virus strain 385-99 isol...		44.1	0.004
<a href="#">gi 77853218 gb AY848697.2 </a>	West Nile virus strain 385-99 isol...		44.1	0.004
<a href="#">gi 66735926 gb DQ066423.1 </a>	West Nile virus strain 385-99 isol...		44.1	0.004
<a href="#">gi 75859185 gb AY842931.3 </a>	West Nile virus strain 385-99, comple		44.1	0.004
<a href="#">gi 77166600 gb DQ211652.1 </a>	West Nile virus strain NY99, complete		44.1	0.004
<a href="#">gi 33242576 gb AY268133.1 </a>	West Nile virus strain PaH001 poly...		44.1	0.004
<a href="#">gi 89148117 gb DQ118127.1 </a>	West Nile virus isolate goose-Hungary		44.1	0.004
<a href="#">gi 21929238 gb AF404756.1 </a>	West Nile virus isolate WN NY 2000-cr		44.1	0.004
<a href="#">gi 21929236 gb AF404755.1 </a>	West Nile virus isolate WN NY 2000-gr		44.1	0.004
<a href="#">gi 21929234 gb AF404754.1 </a>	West Nile virus isolate WN NJ 2000 MQ		44.1	0.004
<a href="#">gi 21929232 gb AF404753.1 </a>	West Nile virus isolate WN MD 2000-cr		44.1	0.004
<a href="#">gi 19387527 gb AF481864.1 </a>	West Nile virus strain IS-98 STD, com		44.1	0.004
<a href="#">gi 89340786 gb DQ411035.1 </a>	West Nile virus isolate Ast02-2-692,		44.1	0.004
<a href="#">gi 89340784 gb DQ411034.1 </a>	West Nile virus isolate Ast02-2-691,		44.1	0.004
<a href="#">gi 89340782 gb DQ411033.1 </a>	West Nile virus isolate Ast02-3-165,		44.1	0.004
<a href="#">gi 89340780 gb DQ411032.1 </a>	West Nile virus isolate Ast02-3-146,		44.1	0.004
<a href="#">gi 89340778 gb DQ411031.1 </a>	West Nile virus isolate Ast01-187, co		44.1	0.004
<a href="#">gi 89340495 gb DQ411030.1 </a>	West Nile virus isolate Ast01-182, co		44.1	0.004
<a href="#">gi 89340493 gb DQ411029.1 </a>	West Nile virus isolate Ast01-66, com		44.1	0.004
<a href="#">gi 19421851 gb AF375044.1 </a>	West Nile virus isolate WN_0247 polyp		44.1	0.004
<a href="#">gi 19421847 gb AF375042.1 </a>	West Nile virus isolate WN_0043 polyp		44.1	0.004
<a href="#">gi 17226060 gb AF375223.1 </a>	AF375223 West Nile virus polyprotein g		44.1	0.004
<a href="#">gi 87116126 gb DQ377180.1 </a>	West Nile virus isolate Ast02-3-208,		44.1	0.004
<a href="#">gi 87116124 gb DQ377179.1 </a>	West Nile virus isolate Ast02-2-298,		44.1	0.004
<a href="#">gi 87116122 gb DQ377178.1 </a>	West Nile virus isolate Ast02-2-26, c		44.1	0.004
<a href="#">gi 87083864 gb DQ374653.1 </a>	West Nile virus isolate Ast02-2-25, c		44.1	0.004
<a href="#">gi 87083862 gb DQ374652.1 </a>	West Nile virus isolate Ast04-2-824A,		44.1	0.004
<a href="#">gi 87083860 gb DQ374651.1 </a>	West Nile virus isolate Ast02-3-570,		44.1	0.004
<a href="#">gi 87083858 gb DQ374650.1 </a>	West Nile virus isolate Ast02-3-717,		44.1	0.004
<a href="#">gi 30349729 gb AY278441.1 </a>	West Nile virus isolate Ast99-901, co		44.1	0.004
<a href="#">gi 51318183 gb AY603654.1 </a>	West Nile virus strain EthAn4766, com		44.1	0.004
<a href="#">gi 55669121 gb AY646354.1 </a>	West Nile virus from USA, complete ge		44.1	0.004
<a href="#">gi 50872125 dbj AB185915.2 </a>	West Nile virus gene for polyprot...		44.1	0.004
<a href="#">gi 50872124 dbj AB185914.2 </a>	West Nile virus gene for polyprot...		44.1	0.004
<a href="#">gi 50838784 dbj AB185917.1 </a>	West Nile virus gene for polyprot...		44.1	0.004
<a href="#">gi 50838782 dbj AB185916.1 </a>	West Nile virus gene for polyprot...		44.1	0.004
<a href="#">gi 11597239 gb AF196835.2 </a>	AF196835 West Nile virus strain NY99-f		44.1	0.004

<a href="#">gi 71483642 gb DQ080072.1 </a>	West Nile virus isolate FL232 poly...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483640 gb DQ080071.1 </a>	West Nile virus isolate FL234 poly...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483638 gb DQ080070.1 </a>	West Nile virus isolate TVP9115 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483636 gb DQ080069.1 </a>	West Nile virus isolate TVP9117 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483634 gb DQ080068.1 </a>	West Nile virus isolate TVP9218 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483632 gb DQ080067.1 </a>	West Nile virus isolate TVP9219 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483630 gb DQ080066.1 </a>	West Nile virus isolate TVP9220 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483628 gb DQ080065.1 </a>	West Nile virus isolate TVP9221 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483626 gb DQ080064.1 </a>	West Nile virus isolate TVP9222 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483624 gb DQ080063.1 </a>	West Nile virus isolate TVP9223 po...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483622 gb DQ080062.1 </a>	West Nile virus isolate TWN165 pol...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483620 gb DQ080061.1 </a>	West Nile virus isolate TWN496 pol...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483618 gb DQ080060.1 </a>	West Nile virus isolate WNVcc poly...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483616 gb DQ080059.1 </a>	West Nile virus isolate L-CA-04 SA...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483614 gb DQ080058.1 </a>	West Nile virus isolate J-CA-03 Ar...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483612 gb DQ080057.1 </a>	West Nile virus isolate I-CA-03 Ar...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483610 gb DQ080056.1 </a>	West Nile virus isolate G-CA-03 IM...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483608 gb DQ080055.1 </a>	West Nile virus isolate F-CA-03 IM...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483606 gb DQ080054.1 </a>	West Nile virus isolate E-CA-03 GR...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483604 gb DQ080053.1 </a>	West Nile virus isolate C-AZ-03 03...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483602 gb DQ080052.1 </a>	West Nile virus isolate B-AZ-03-16...	<a href="#">44.1</a>	0.004
<a href="#">gi 71483600 gb DQ080051.1 </a>	West Nile virus isolate A-AZ-03-16...	<a href="#">44.1</a>	0.004
<a href="#">gi 9930133 gb AF260967.1 AF260967</a>	West Nile virus strain NY99-eq	<a href="#">44.1</a>	0.004
<a href="#">gi 26284711 gb AF533540.1 </a>	West Nile virus polyprotein precursor	<a href="#">44.1</a>	0.004
<a href="#">gi 77172001 gb AF206518.2 AF206518</a>	West Nile virus isolate 2741,	<a href="#">44.1</a>	0.004
<a href="#">gi 6715269 gb AF194117.1 AF194117</a>	West Nile virus structural pro	<a href="#">44.1</a>	0.004
<a href="#">gi 6581069 gb AF202541.1 AF202541</a>	West Nile virus strain HNY1...	<a href="#">44.1</a>	0.004
<a href="#">gi 33948906 gb AY289214.1 </a>	West Nile virus strain TVP 8533 compl	<a href="#">44.1</a>	0.004
<a href="#">gi 59876232 gb AY795965.1 </a>	West Nile virus isolate ARC10, comple	<a href="#">44.1</a>	0.004
<a href="#">gi 58618098 gb AY839588.1 </a>	West Nile virus strain MgAn 786/6/...	<a href="#">44.1</a>	0.004
<a href="#">gi 76781571 gb DQ164206.1 </a>	West Nile virus isolate TX 2004 Harri	<a href="#">44.1</a>	0.004
<a href="#">gi 76781569 gb DQ164205.1 </a>	West Nile virus isolate TX 2002 2, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781567 gb DQ164204.1 </a>	West Nile virus isolate CO 2003 1, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781565 gb DQ164203.1 </a>	West Nile virus isolate CO 2003 2, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781563 gb DQ164202.1 </a>	West Nile virus isolate OH 2002, comp	<a href="#">44.1</a>	0.004
<a href="#">gi 76781561 gb DQ164201.1 </a>	West Nile virus isolate AZ 2004, comp	<a href="#">44.1</a>	0.004
<a href="#">gi 76781559 gb DQ164200.1 </a>	West Nile virus isolate IN 2002, comp	<a href="#">44.1</a>	0.004
<a href="#">gi 76781557 gb DQ164199.1 </a>	West Nile virus isolate TX 2003, comp	<a href="#">44.1</a>	0.004
<a href="#">gi 76781555 gb DQ164198.1 </a>	West Nile virus isolate TX 2002 1, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781553 gb DQ164197.1 </a>	West Nile virus isolate GA 2002 2, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781551 gb DQ164196.1 </a>	West Nile virus isolate GA 2002 1, co	<a href="#">44.1</a>	0.004
<a href="#">gi 76781549 gb DQ164195.1 </a>	West Nile virus isolate NY 2002 Nassa	<a href="#">44.1</a>	0.004
<a href="#">gi 76781547 gb DQ164194.1 </a>	West Nile virus isolate NY 2001 Suffo	<a href="#">44.1</a>	0.004
<a href="#">gi 76781545 gb DQ164193.1 </a>	West Nile virus isolate NY 2002 Clint	<a href="#">44.1</a>	0.004
<a href="#">gi 76781543 gb DQ164192.1 </a>	West Nile virus isolate NY 2003 Rockl	<a href="#">44.1</a>	0.004
<a href="#">gi 76781541 gb DQ164191.1 </a>	West Nile virus isolate NY 2003 Chaut	<a href="#">44.1</a>	0.004
<a href="#">gi 76781539 gb DQ164190.1 </a>	West Nile virus isolate NY 2003 Suffo	<a href="#">44.1</a>	0.004
<a href="#">gi 76781537 gb DQ164189.1 </a>	West Nile virus isolate NY 2003 Alban	<a href="#">44.1</a>	0.004
<a href="#">gi 76781535 gb DQ164188.1 </a>	West Nile virus isolate NY 2003 Westc	<a href="#">44.1</a>	0.004
<a href="#">gi 76781533 gb DQ164187.1 </a>	West Nile virus isolate NY 2002 Broom	<a href="#">44.1</a>	0.004
<a href="#">gi 76781531 gb DQ164186.1 </a>	West Nile virus isolate NY 2002 Queen	<a href="#">44.1</a>	0.004
<a href="#">gi 46277828 gb AY490240.2 </a>	West Nile virus strain Chin-01, compl	<a href="#">42.1</a>	0.014
<a href="#">gi 33242574 gb AY268132.1 </a>	West Nile virus strain PaAn001 pol...	<a href="#">42.1</a>	0.014
<a href="#">gi 30230630 gb AY262283.1 </a>	West Nile virus isolate KN3829 polypr	<a href="#">42.1</a>	0.014
<a href="#">gi 21929240 gb AF404757.1 </a>	West Nile virus isolate WN Italy 1998	<a href="#">42.1</a>	0.014
<a href="#">gi 19421853 gb AF375045.1 </a>	West Nile virus isolate WN_0304 polyp	<a href="#">42.1</a>	0.014

## Alignments

> ☐ [gi|55975602|gb|AY660002.1|](#) ☒ West Nile virus isolate Mex03 from Mexico, complete ge  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> ☐ [gi|55495180|gb|AY712948.1|](#) ☒ West Nile virus isolate Mosquito v4369, complete genor  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> ☐ [gi|55495165|gb|AY712947.1|](#) ☒ West Nile virus isolate Bird 1461, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> ☐ [gi|55495149|gb|AY712946.1|](#) ☒ West Nile virus isolate Bird 1171, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> ☐ [gi|55495130|gb|AY712945.1|](#) ☒ West Nile virus isolate Bird 1153, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
```

Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|51095221|gb|AY688948.1| **D** West Nile virus strain Sarafend, complete genome  
Length=11057

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77980183|gb|AY848696.2| **D** West Nile virus strain 385-99 isolate hamster passage  
9317E, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77980181|gb|AY848695.2| **D** West Nile virus strain 385-99 isolate hamster passage  
9317A, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77853218|gb|AY848697.2| **D** West Nile virus strain 385-99 isolate hamster passage  
TVP-9376, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|66735926|gb|DQ066423.1| **D** West Nile virus strain 385-99 isolate hamster passage  
9317B, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)

. Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|75859185|gb|AY842931.3|](#) **D** West Nile virus strain 385-99, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|77166600|gb|DQ211652.1|](#) **D** West Nile virus strain NY99, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|33242576|gb|AY268133.1|](#) **D** West Nile virus strain PaH001 polyprotein (pol) gene,  
cds  
Length=10989

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 175    AGCCCTCTTCAGTCCAATCAAG  154
```

> [gi|89148117|gb|DQ118127.1|](#) **D** West Nile virus isolate goose-Hungary/03, complete ger  
Length=10969

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|21929238|gb|AF404756.1|](#) **D** West Nile virus isolate WN NY 2000-crow3356, complete  
Length=11029

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> gi|21929236|gb|AF404755.1| **D** West Nile virus isolate WN NY 2000-grouse3282, complete  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> gi|21929234|gb|AF404754.1| **D** West Nile virus isolate WN NJ 2000 MQ5488, complete ge  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> gi|21929232|gb|AF404753.1| **D** West Nile virus isolate WN MD 2000-crow265, complete  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> gi|19387527|gb|AF481864.1| **D** West Nile virus strain IS-98 STD, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> gi|89340786|gb|DQ411035.1| **D** West Nile virus isolate Ast02-2-692, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004



Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340784|gb|DQ411034.1|](#) **D** West Nile virus isolate Ast02-2-691, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340782|gb|DQ411033.1|](#) **D** West Nile virus isolate Ast02-3-165, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340780|gb|DQ411032.1|](#) **D** West Nile virus isolate Ast02-3-146, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340778|gb|DQ411031.1|](#) **D** West Nile virus isolate Ast01-187, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340495|gb|DQ411030.1|](#) **D** West Nile virus isolate Ast01-182, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340493|gb|DQ411029.1|](#) **D** West Nile virus isolate Ast01-66, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|19421851|gb|AF375044.1|](#) West Nile virus isolate WN\_0247 polyprotein mRNA, partial  
Length=1648

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|19421847|gb|AF375042.1|](#) West Nile virus isolate WN\_0043 polyprotein mRNA, partial  
Length=1648

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|17226060|gb|AF375223.1|AF375223](#) West Nile virus polyprotein gene, partial cds  
Length=1648

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|87116126|gb|DQ377180.1|](#) **D** West Nile virus isolate Ast02-3-208, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87116124|gb|DQ377179.1|](#) **D** West Nile virus isolate Ast02-2-298, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87116122|gb|DQ377178.1|](#) **D** West Nile virus isolate Ast02-2-26, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87083864|gb|DQ374653.1|](#) **D** West Nile virus isolate Ast02-2-25, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87083862|gb|DQ374652.1|](#) **D** West Nile virus isolate Ast04-2-824A,, complete genome  
Length=10789

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87083860|gb|DQ374651.1|](#) **D** West Nile virus isolate Ast02-3-570, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87083858|gb|DQ374650.1](#) **D** West Nile virus isolate Ast02-3-717, complete genome  
Length=10811

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|30349729|gb|AY278441.1](#) **D** West Nile virus isolate Ast99-901, complete genome  
Length=10998

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|51318183|gb|AY603654.1](#) **D** West Nile virus strain EthAn4766, complete genome  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|55669121|gb|AY646354.1](#) **D** West Nile virus from USA, complete genome  
Length=11030

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50872125|dbj|AB185915.2](#) **D** West Nile virus gene for polyprotein precursor prote:  
cds, isolate: 6-SP  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50872124|dbj|AB185914.2|](#) **D** West Nile virus gene for polyprotein precursor protei  
cds, isolate: 6-LP  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50838784|dbj|AB185917.1|](#) **D** West Nile virus gene for polyprotein precursor protei  
cds, isolate: B-LP  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50838782|dbj|AB185916.1|](#) **D** West Nile virus gene for polyprotein precursor protei  
cds, isolate: B-SP  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|11597239|gb|AF196835.2|AF196835](#) **D** West Nile virus strain NY99-flamingo382-99, co  
Length=11029

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|71483642|gb|DQ080072.1| **D** West Nile virus isolate FL232 polyprotein precursor, complete cds  
Length=11000

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 166 AGCCCTCTTCAGTCCAATCAAG 145

> gi|71483640|gb|DQ080071.1| **D** West Nile virus isolate FL234 polyprotein precursor, complete cds  
Length=11000

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 166 AGCCCTCTTCAGTCCAATCAAG 145

> gi|71483638|gb|DQ080070.1| **D** West Nile virus isolate TVP9115 polyprotein precursor, complete cds  
Length=11001

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 167 AGCCCTCTTCAGTCCAATCAAG 146

> gi|71483636|gb|DQ080069.1| **D** West Nile virus isolate TVP9117 polyprotein precursor, complete cds  
Length=10975

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22  
|||||  
Sbjct 167 AGCCCTCTTCAGTCCAATCAAG 146

> gi|71483634|gb|DQ080068.1| **D** West Nile virus isolate TVP9218 polyprotein precursor, complete cds  
Length=11001

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```

Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 167    AGCCCTCTTCAGTCCAATCAAG  146

```

> [gi|71483632|gb|DQ080067.1|](#) **D** West Nile virus isolate TVP9219 polyprotein precursor, complete cds  
Length=11001

Score = 44.1 bits (22), Expect = 0.004  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```

Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 167    AGCCCTCTTCAGTCCAATCAAG  146

```





Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jun 5, 2006 10:17 PM

Number of letters in database: 143,922,531

Number of sequences in database: 3,946,763

Lambda K H  
1.37 0.711 1.31

Gapped

Lambda K H  
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 3946763

Number of Hits to DB: 272830

Number of extensions: 10932

Number of successful extensions: 10932

Number of sequences better than 10: 23

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 10932

Number of HSP's successfully gapped: 23

Length of query: 22

Length of database: 17323791715

Length adjustment: 18

Effective length of query: 4

Effective length of database: 17252749981

Effective search space: 69010999924

Effective search space used: 69010999924

A: 0

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 11 (22.3 bits)

S2: 17 (34.2 bits)



# results of BLAST

BLASTN 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1149884457-23746-93944912608.BLASTQ4

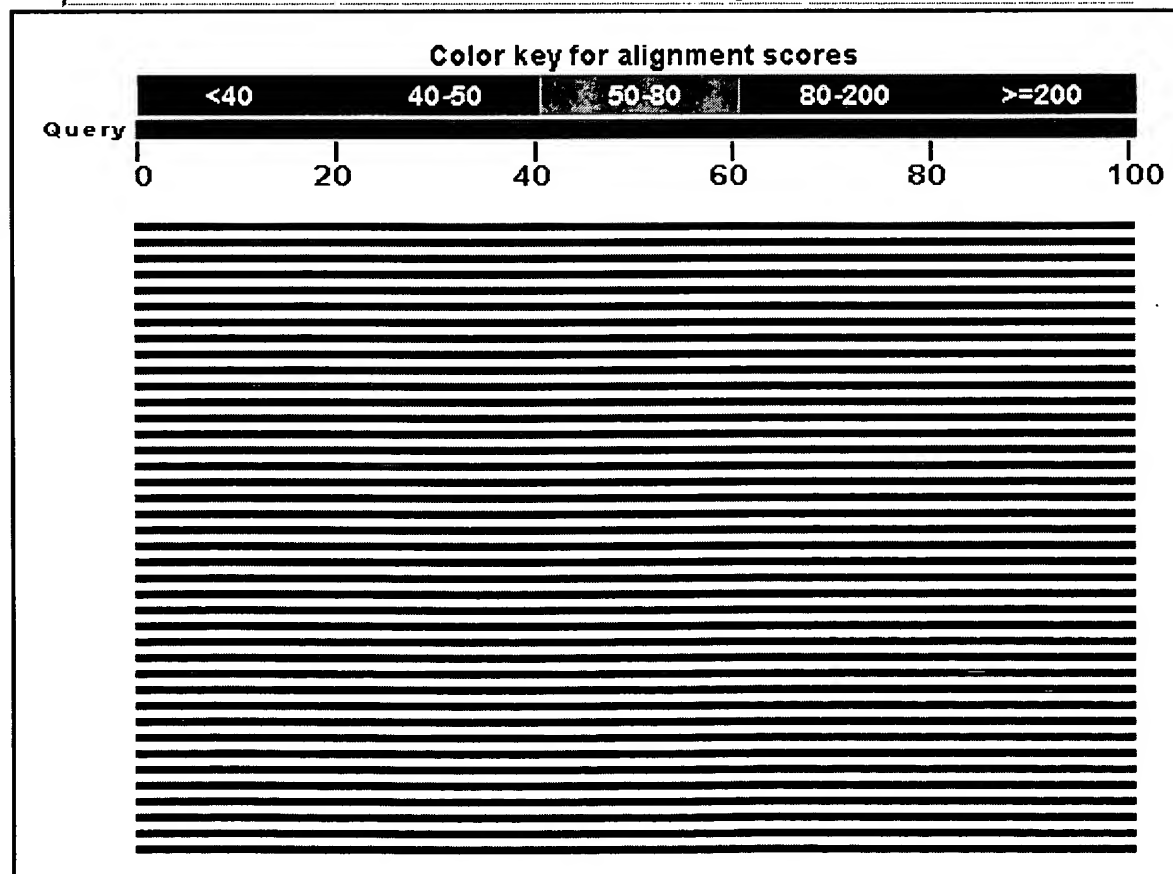
**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
3,946,763 sequences; 17,323,791,715 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

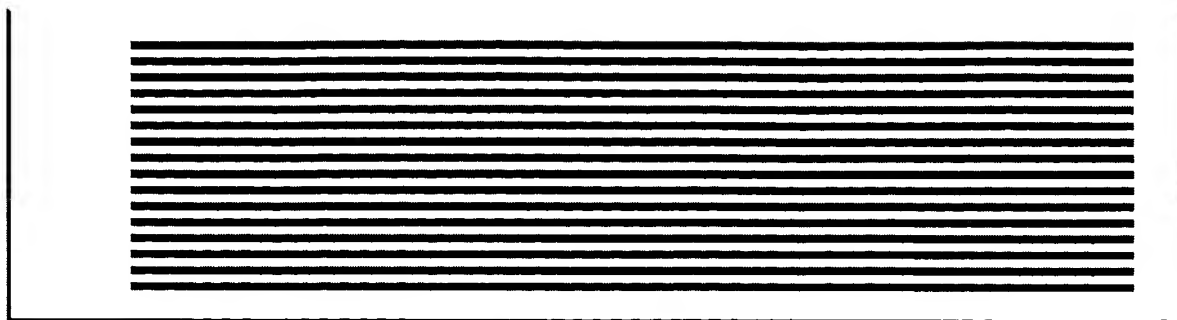
**Query=**  
Length=101

## Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments







Tree view 

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 55975602 gb AY660002.1 </a>	West Nile virus isolate Mex03 from Me		<a href="#">200</a>	5e-49
<a href="#">gi 55495180 gb AY712948.1 </a>	West Nile virus isolate Mosquito v436		<a href="#">200</a>	5e-49
<a href="#">gi 55495165 gb AY712947.1 </a>	West Nile virus isolate Bird 1461, co		<a href="#">200</a>	5e-49
<a href="#">gi 55495149 gb AY712946.1 </a>	West Nile virus isolate Bird 1171, co		<a href="#">200</a>	5e-49
<a href="#">gi 55495130 gb AY712945.1 </a>	West Nile virus isolate Bird 1153, co		<a href="#">200</a>	5e-49
<a href="#">gi 77980183 gb AY848696.2 </a>	West Nile virus strain 385-99 isol...		<a href="#">200</a>	5e-49
<a href="#">gi 77980181 gb AY848695.2 </a>	West Nile virus strain 385-99 isol...		<a href="#">200</a>	5e-49
<a href="#">gi 77853218 gb AY848697.2 </a>	West Nile virus strain 385-99 isol...		<a href="#">200</a>	5e-49
<a href="#">gi 66735926 gb DQ066423.1 </a>	West Nile virus strain 385-99 isol...		<a href="#">200</a>	5e-49
<a href="#">gi 75859185 gb AY842931.3 </a>	West Nile virus strain 385-99, comple		<a href="#">200</a>	5e-49
<a href="#">gi 77166600 gb DQ211652.1 </a>	West Nile virus strain NY99, complete		<a href="#">200</a>	5e-49
<a href="#">gi 46277828 gb AY490240.2 </a>	West Nile virus strain Chin-01, compl		<a href="#">200</a>	5e-49
<a href="#">gi 33242576 gb AY268133.1 </a>	West Nile virus strain PaH001 poly...		<a href="#">200</a>	5e-49
<a href="#">gi 33242574 gb AY268132.1 </a>	West Nile virus strain PaAn001 pol...		<a href="#">200</a>	5e-49
<a href="#">gi 89148117 gb DQ118127.1 </a>	West Nile virus isolate goose-Hungary		<a href="#">200</a>	5e-49
<a href="#">gi 21929240 gb AF404757.1 </a>	West Nile virus isolate WN Italy 1998		<a href="#">200</a>	5e-49
<a href="#">gi 21929238 gb AF404756.1 </a>	West Nile virus isolate WN NY 2000-cr		<a href="#">200</a>	5e-49
<a href="#">gi 21929234 gb AF404754.1 </a>	West Nile virus isolate WN NJ 2000 MQ		<a href="#">200</a>	5e-49
<a href="#">gi 21929232 gb AF404753.1 </a>	West Nile virus isolate WN MD 2000-cr		<a href="#">200</a>	5e-49
<a href="#">gi 19387527 gb AF481864.1 </a>	West Nile virus strain IS-98 STD, com		<a href="#">200</a>	5e-49
<a href="#">gi 30349731 gb AY278442.1 </a>	West Nile virus isolate LEIV-Vlg00-27		<a href="#">200</a>	5e-49
<a href="#">gi 30349727 gb AY277252.1 </a>	West Nile virus isolate LEIV-Vlg99-27		<a href="#">200</a>	5e-49
<a href="#">gi 51318183 gb AY603654.1 </a>	West Nile virus strain EthAn4766, com		<a href="#">200</a>	5e-49
<a href="#">gi 50872125 dbj AB185915.2 </a>	West Nile virus gene for polyprot...		<a href="#">200</a>	5e-49
<a href="#">gi 50872124 dbj AB185914.2 </a>	West Nile virus gene for polyprot...		<a href="#">200</a>	5e-49
<a href="#">gi 50838784 dbj AB185917.1 </a>	West Nile virus gene for polyprot...		<a href="#">200</a>	5e-49
<a href="#">gi 50838782 dbj AB185916.1 </a>	West Nile virus gene for polyprot...		<a href="#">200</a>	5e-49
<a href="#">gi 12744408 gb AF317203.1 AF317203</a>	West Nile virus VLG-4 polypro		<a href="#">200</a>	5e-49
<a href="#">gi 11597239 gb AF196835.2 AF196835</a>	West Nile virus strain NY99-f		<a href="#">200</a>	5e-49
<a href="#">gi 71483642 gb DQ080072.1 </a>	West Nile virus isolate FL232 poly...		<a href="#">200</a>	5e-49
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<a href="#">gi 71483638 gb DQ080070.1 </a>	West Nile virus isolate TVP9115 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483636 gb DQ080069.1 </a>	West Nile virus isolate TVP9117 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483634 gb DQ080068.1 </a>	West Nile virus isolate TVP9218 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483632 gb DQ080067.1 </a>	West Nile virus isolate TVP9219 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483630 gb DQ080066.1 </a>	West Nile virus isolate TVP9220 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483628 gb DQ080065.1 </a>	West Nile virus isolate TVP9221 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483626 gb DQ080064.1 </a>	West Nile virus isolate TVP9222 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483624 gb DQ080063.1 </a>	West Nile virus isolate TVP9223 po...		<a href="#">200</a>	5e-49
<a href="#">gi 71483622 gb DQ080062.1 </a>	West Nile virus isolate TWN165 pol...		<a href="#">200</a>	5e-49
<a href="#">gi 71483620 gb DQ080061.1 </a>	West Nile virus isolate TWN496 pol...		<a href="#">200</a>	5e-49
<a href="#">gi 71483616 gb DQ080059.1 </a>	West Nile virus isolate L-CA-04 SA...		<a href="#">200</a>	5e-49
<a href="#">gi 71483614 gb DQ080058.1 </a>	West Nile virus isolate J-CA-03 Ar...		<a href="#">200</a>	5e-49
<a href="#">gi 71483612 gb DQ080057.1 </a>	West Nile virus isolate I-CA-03 Ar...		<a href="#">200</a>	5e-49

<a href="#">gi 71483610 gb DQ080056.1 </a>	West Nile virus isolate G-CA-03 IM...	<a href="#">200</a>	5e-49
<a href="#">gi 71483608 gb DQ080055.1 </a>	West Nile virus isolate F-CA-03 IM...	<a href="#">200</a>	5e-49
<a href="#">gi 71483606 gb DQ080054.1 </a>	West Nile virus isolate E-CA-03 GR...	<a href="#">200</a>	5e-49
<a href="#">gi 71483604 gb DQ080053.1 </a>	West Nile virus isolate C-AZ-03 03...	<a href="#">200</a>	5e-49
<a href="#">gi 71483602 gb DQ080052.1 </a>	West Nile virus isolate B-AZ-03-16...	<a href="#">200</a>	5e-49
<a href="#">gi 71483600 gb DQ080051.1 </a>	West Nile virus isolate A-AZ-03-16...	<a href="#">200</a>	5e-49
<a href="#">gi 9930137 gb AF260969.1 AF260969</a>	West Nile virus strain RO97-50	<a href="#">200</a>	5e-49
<a href="#">gi 9930135 gb AF260968.1 AF260968</a>	West Nile virus strain Eg101,	<a href="#">200</a>	5e-49
<a href="#">gi 9930133 gb AF260967.1 AF260967</a>	West Nile virus strain NY99-eq	<a href="#">200</a>	5e-49
<a href="#">gi 26284711 gb AF533540.1 </a>	West Nile virus polyprotein precursor	<a href="#">200</a>	5e-49
<a href="#">gi 7717200 gb AF206518.2 AF206518</a>	West Nile virus isolate 2741,	<a href="#">200</a>	5e-49
<a href="#">gi 6581069 gb AF202541.1 AF202541</a>	West Nile virus strain HNY1...	<a href="#">200</a>	5e-49
<a href="#">gi 33948906 gb AY289214.1 </a>	West Nile virus strain TVP 8533 compl	<a href="#">200</a>	5e-49
<a href="#">gi 59876232 gb AY795965.1 </a>	West Nile virus isolate ARC10, comple	<a href="#">200</a>	5e-49
<a href="#">gi 51011375 gb AY701413.1 </a>	West Nile virus strain 04.05 polyprot	<a href="#">200</a>	5e-49
<a href="#">gi 51011373 gb AY701412.1 </a>	West Nile virus strain 96-111 polypro	<a href="#">200</a>	5e-49
<a href="#">gi 76781571 gb DQ164206.1 </a>	West Nile virus isolate TX 2004 Harri	<a href="#">200</a>	5e-49
<a href="#">gi 76781567 gb DQ164204.1 </a>	West Nile virus isolate CO 2003 1, co	<a href="#">200</a>	5e-49
<a href="#">gi 76781565 gb DQ164203.1 </a>	West Nile virus isolate CO 2003 2, co	<a href="#">200</a>	5e-49
<a href="#">gi 76781563 gb DQ164202.1 </a>	West Nile virus isolate OH 2002, comp	<a href="#">200</a>	5e-49
<a href="#">gi 76781561 gb DQ164201.1 </a>	West Nile virus isolate AZ 2004, comp	<a href="#">200</a>	5e-49
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<a href="#">gi 76781557 gb DQ164199.1 </a>	West Nile virus isolate TX 2003, comp	<a href="#">200</a>	5e-49
<a href="#">gi 76781553 gb DQ164197.1 </a>	West Nile virus isolate GA 2002 2, co	<a href="#">200</a>	5e-49
<a href="#">gi 76781551 gb DQ164196.1 </a>	West Nile virus isolate GA 2002 1, co	<a href="#">200</a>	5e-49
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<a href="#">gi 76781547 gb DQ164194.1 </a>	West Nile virus isolate NY 2001 Suffo	<a href="#">200</a>	5e-49
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<a href="#">gi 76781543 gb DQ164192.1 </a>	West Nile virus isolate NY 2003 Rockl	<a href="#">200</a>	5e-49
<a href="#">gi 76781541 gb DQ164191.1 </a>	West Nile virus isolate NY 2003 Chaut	<a href="#">200</a>	5e-49
<a href="#">gi 76781539 gb DQ164190.1 </a>	West Nile virus isolate NY 2003 Suffo	<a href="#">200</a>	5e-49
<a href="#">gi 76781537 gb DQ164189.1 </a>	West Nile virus isolate NY 2003 Alban	<a href="#">200</a>	5e-49
<a href="#">gi 76781535 gb DQ164188.1 </a>	West Nile virus isolate NY 2003 Westc	<a href="#">200</a>	5e-49
<a href="#">gi 76781533 gb DQ164187.1 </a>	West Nile virus isolate NY 2002 Broom	<a href="#">200</a>	5e-49
<a href="#">gi 76781531 gb DQ164186.1 </a>	West Nile virus isolate NY 2002 Queen	<a href="#">200</a>	5e-49
<a href="#">gi 30230630 gb AY262283.1 </a>	West Nile virus isolate KN3829 polypr	<a href="#">192</a>	1e-46
<a href="#">gi 21929236 gb AF404755.1 </a>	West Nile virus isolate WN NY 2000-gr	<a href="#">192</a>	1e-46
<a href="#">gi 89340786 gb DQ411035.1 </a>	West Nile virus isolate Ast02-2-692,	<a href="#">192</a>	1e-46
<a href="#">gi 89340784 gb DQ411034.1 </a>	West Nile virus isolate Ast02-2-691,	<a href="#">192</a>	1e-46
<a href="#">gi 89340780 gb DQ411032.1 </a>	West Nile virus isolate Ast02-3-146,	<a href="#">192</a>	1e-46
<a href="#">gi 89340778 gb DQ411031.1 </a>	West Nile virus isolate Ast01-187, co	<a href="#">192</a>	1e-46
<a href="#">gi 89340495 gb DQ411030.1 </a>	West Nile virus isolate Ast01-182, co	<a href="#">192</a>	1e-46
<a href="#">gi 89340493 gb DQ411029.1 </a>	West Nile virus isolate Ast01-66, com	<a href="#">192</a>	1e-46
<a href="#">gi 87116126 gb DQ377180.1 </a>	West Nile virus isolate Ast02-3-208,	<a href="#">192</a>	1e-46
<a href="#">gi 87116124 gb DQ377179.1 </a>	West Nile virus isolate Ast02-2-298,	<a href="#">192</a>	1e-46
<a href="#">gi 87116122 gb DQ377178.1 </a>	West Nile virus isolate Ast02-2-26, c	<a href="#">192</a>	1e-46
<a href="#">gi 87083864 gb DQ374653.1 </a>	West Nile virus isolate Ast02-2-25, c	<a href="#">192</a>	1e-46
<a href="#">gi 87083862 gb DQ374652.1 </a>	West Nile virus isolate Ast04-2-824A,	<a href="#">192</a>	1e-46
<a href="#">gi 87083860 gb DQ374651.1 </a>	West Nile virus isolate Ast02-3-570,	<a href="#">192</a>	1e-46
<a href="#">gi 87083858 gb DQ374650.1 </a>	West Nile virus isolate Ast02-3-717,	<a href="#">192</a>	1e-46
<a href="#">gi 30349729 gb AY278441.1 </a>	West Nile virus isolate Ast99-901, co	<a href="#">192</a>	1e-46
<a href="#">gi 55669121 gb AY646354.1 </a>	West Nile virus from USA, complete ge	<a href="#">192</a>	1e-46
<a href="#">gi 71483618 gb DQ080060.1 </a>	West Nile virus isolate WNVCC poly...	<a href="#">192</a>	1e-46
<a href="#">gi 76781569 gb DQ164205.1 </a>	West Nile virus isolate TX 2002 2, co	<a href="#">192</a>	1e-46
<a href="#">gi 76781555 gb DQ164198.1 </a>	West Nile virus isolate TX 2002 1, co	<a href="#">192</a>	1e-46
<a href="#">gi 89340782 gb DQ411033.1 </a>	West Nile virus isolate Ast02-3-165,	<a href="#">184</a>	3e-44

## Alignments

> ☐ [gi|55975602|gb|AY660002.1|](#) ☒ West Nile virus isolate Mex03 from Mexico, complete ge  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> ☐ [gi|55495180|gb|AY712948.1|](#) ☒ West Nile virus isolate Mosquito v4369, complete genor  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> ☐ [gi|55495165|gb|AY712947.1|](#) ☒ West Nile virus isolate Bird 1461, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> ☐ [gi|55495149|gb|AY712946.1|](#) ☒ West Nile virus isolate Bird 1171, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
```

```
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  101
          |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  189
```

> [gi|55495130|gb|AY712945.1](#) **D** West Nile virus isolate Bird 1153, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  60
          |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  101
          |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  189
```

> [gi|77980183|gb|AY848696.2](#) **D** West Nile virus strain 385-99 isolate hamster passage  
9317E, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  60
          |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  101
          |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  189
```

> [gi|77980181|gb|AY848695.2](#) **D** West Nile virus strain 385-99 isolate hamster passage  
9317A, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  60
          |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA  148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  101
          |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG  189
```

> [gi|77853218|gb|AY848697.2](#) **D** West Nile virus strain 385-99 isolate hamster passage  
TVP-9376, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|66735926|gb|DQ066423.1](#) **D** West Nile virus strain 385-99 isolate hamster passage 9317B, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|75859185|gb|AY842931.3](#) **D** West Nile virus strain 385-99, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```



> [gi|77166600|gb|DQ211652.1](#) **D** West Nile virus strain NY99, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
```



Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189

>  [gi|46277828|gb|AY490240.2|](#)  West Nile virus strain Chin-01, complete genome  
Length=11028

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 89   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 149   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|33242576|gb|AY268133.1|](#)  West Nile virus strain PaH001 polyprotein (pol) gene,  
cds  
Length=10989

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 69   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 128



Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 129   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 169
```

>  [gi|33242574|gb|AY268132.1|](#)  West Nile virus strain PaAn001 polyprotein (pol) gene,  
cds  
Length=10989

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 69   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 128

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 129   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 169
```

>  [gi|89148117|gb|DQ118127.1|](#)  West Nile virus isolate goose-Hungary/03, complete genome  
Length=10969

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
            |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
            |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929240|gb|AF404757.1](#) **D** West Nile virus isolate WN Italy 1998-equine, complete  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
            |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
            |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929238|gb|AF404756.1](#) **D** West Nile virus isolate WN NY 2000-crow3356, complete  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
            |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
            |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929234|gb|AF404754.1](#) **D** West Nile virus isolate WN NJ 2000 MQ5488, complete ge  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
            |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
            |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929232|gb|AF404753.1](#) **D** West Nile virus isolate WN MD 2000-crow265, complete c  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|19387527|gb|AF481864.1](#) **D** West Nile virus strain IS-98 STD, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|30349731|gb|AY278442.1](#) **D** West Nile virus isolate LEIV-Vlg00-27924, complete ger  
Length=10842

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```



> [gi|30349727|gb|AY277252.1](#) **D** West Nile virus isolate LEIV-Vlg99-27889, complete ger  
Length=10845

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```





>  [gi|51318183|gb|AY603654.1|](#)  West Nile virus strain EthAn4766, complete genome  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50872125|dbj|AB185915.2|](#)  West Nile virus gene for polyprotein precursor protei:  
cds, isolate: 6-SP  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50872124|dbj|AB185914.2|](#)  West Nile virus gene for polyprotein precursor protei:  
cds, isolate: 6-LP  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50838784|dbj|AB185917.1|](#)  West Nile virus gene for polyprotein precursor protei:  
cds, isolate: B-LP  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
```

```
.
Sbjct  89  |||||
AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|50838782|dbj|AB185916.1|](#) **D** West Nile virus gene for polyprotein precursor protei  
cds, isolate: B-SP  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|12744408|gb|AF317203.1|AF317203](#) **D** West Nile virus VLG-4 polyprotein precursor, c  
Length=10972

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct  57  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 116

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct  117  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 157
```

> [gi|11597239|gb|AF196835.2|AF196835](#) **D** West Nile virus strain NY99-flamingo382-99, c  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483642|gb|DQ080072.1|](#) **D** West Nile virus isolate FL232 polyprotein precursor, c  
cds  
Length=11000

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 60   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 120  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 160
```

> [gi|71483640|gb|DQ080071.1|](#) **D** West Nile virus isolate FL234 polyprotein precursor, complete cds  
Length=11000

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 60   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 120  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 160
```

> [gi|71483638|gb|DQ080070.1|](#) **D** West Nile virus isolate TVP9115 polyprotein precursor, complete cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 121  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483636|gb|DQ080069.1|](#) **D** West Nile virus isolate TVP9117 polyprotein precursor, complete cds  
Length=10975

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120
```

```
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483634|gb|DQ080068.1|](#) **D** West Nile virus isolate TVP9218 polyprotein precursor, complete cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483632|gb|DQ080067.1|](#) **D** West Nile virus isolate TVP9219 polyprotein precursor, complete cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483630|gb|DQ080066.1|](#) **D** West Nile virus isolate TVP9220 polyprotein precursor, complete cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483628|gb|DQ080065.1|](#) **D** West Nile virus isolate TVP9221 polyprotein precursor, complete cds  
Length=10995

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 55  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 114

Query 61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 115 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 155
```

>[gi|71483626|gb|DQ080064.1|](#) **D** West Nile virus isolate TVP9222 polyprotein precursor, complete cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

>[gi|71483624|gb|DQ080063.1|](#) **D** West Nile virus isolate TVP9223 polyprotein precursor, complete cds  
Length=10975

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

>[gi|71483622|gb|DQ080062.1|](#) **D** West Nile virus isolate TWN165 polyprotein precursor, cds  
Length=11001

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
```

|||||  
Sbjct 121 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 161

> gi|71483620|gb|DQ080061.1| **D** West Nile virus isolate TWN496 polyprotein precursor,  
cds  
Length=11000

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60  
|||||  
Sbjct 60 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119  
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101  
|||||  
Sbjct 120 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 160

> gi|71483616|gb|DQ080059.1| **D** West Nile virus isolate L-CA-04 SAC-04-7168 polyprotein  
gene, complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60  
|||||  
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148  
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101  
|||||  
Sbjct 149 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 189

> gi|71483614|gb|DQ080058.1| **D** West Nile virus isolate J-CA-03 Arcadia-S0334814 polyprotein  
precursor, gene, complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60  
|||||  
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148  
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101  
|||||  
Sbjct 149 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 189

> gi|71483612|gb|DQ080057.1| **D** West Nile virus isolate I-CA-03 Arcadia-S0331532 polyprotein  
precursor, gene, complete cds  
Length=10956

Score = 200 bits (101), Expect = 5e-49

Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
           |||
Sbjct 89    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
           |||
Sbjct 149    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483610|gb|DQ080056.1](#) **D** West Nile virus isolate G-CA-03 IMPR-1075 polyprotein gene, complete cds  
Length=11019

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
           |||
Sbjct 89    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
           |||
Sbjct 149    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483608|gb|DQ080055.1](#) **D** West Nile virus isolate F-CA-03 IMPR 102 polyprotein gene, complete cds  
Length=11018

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
           |||
Sbjct 89    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
           |||
Sbjct 149    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483606|gb|DQ080054.1](#) **D** West Nile virus isolate E-CA-03 GRLA-1260 polyprotein gene, complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
           |||
Sbjct 89    AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61    AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
           |||
```

Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189

> [gi|71483604|gb|DQ080053.1|](#) **D** West Nile virus isolate C-AZ-03 03-1799 polyprotein p1  
gene, complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 89   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 149   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483602|gb|DQ080052.1|](#) **D** West Nile virus isolate B-AZ-03-1681 polyprotein p1  
complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 89   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 149   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483600|gb|DQ080051.1|](#) **D** West Nile virus isolate A-AZ-03-1623 polyprotein p1  
complete cds  
Length=11029

Score = 200 bits (101), Expect = 5e-49  
Identities = 101/101 (100%), Gaps = 0/101 (0%)  
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 89   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 149   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

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Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)



Posted date: Jun 5, 2006 10:17 PM  
Number of letters in database: 143,922,531  
Number of sequences in database: 3,946,763  
Lambda K H  
1.37 0.711 1.31  
Gapped  
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Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 3946763  
Number of Hits to DB: 1139647  
Number of extensions: 51199  
Number of successful extensions: 13183  
Number of sequences better than 10: 46  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 13183  
Number of HSP's successfully gapped: 46  
Length of query: 101  
Length of database: 17323791715  
Length adjustment: 21  
Effective length of query: 80  
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Effective search space: 1379272775360  
Effective search space used: 1379272775360  
A: 0  
X1: 11 (21.8 bits)  
X2: 15 (29.7 bits)  
X3: 25 (49.6 bits)  
S1: 12 (24.3 bits)  
S2: 19 (38.2 bits)